```
Alignment:    1549 C2460 6216-99% con
  0.65 % 1549   Bacillus coagulans
  4.84 % 1548   Bacillus oleronius
  5.36 % 1550   Bacillus smithii
  5.62 % 1548   Bacillus sporothermodurans
  5.65 % 1551   Bacillus badius
  5.79 % 1547   Bacillus firmus
  5.85 % 1547   Bacillus lentus
  5.90 % 1543   Bacillus circulans
  5.95 % 1545   Bacillus niacini
  6.30 % 1548   Bacillus flexus
```

Neighbor Joining Tree
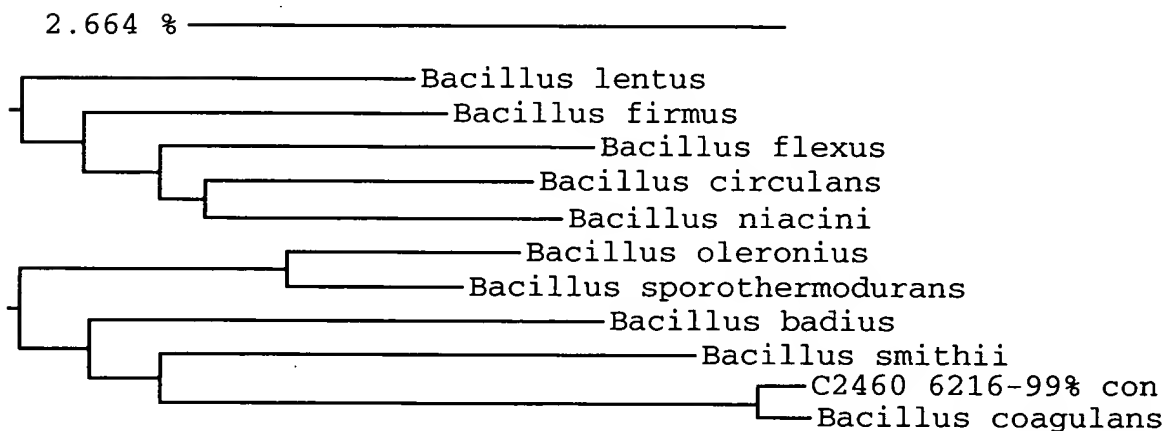
Concise Alignment

```
                      1
                111222222241
                347011256784
                902967240204
C2460 6216-99% con TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)
```

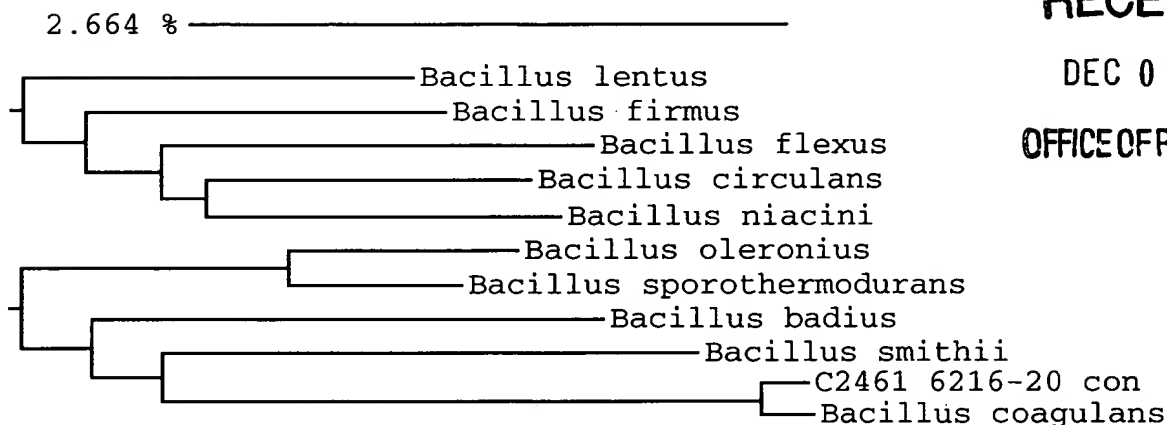# Fig. 6

Fig. 7

```
Alignment:      1549 C2461 6216-20 con
  0.65 % 1549   Bacillus  coagulans
  4.84 % 1548   Bacillus  oleronius
  5.36 % 1550   Bacillus  smithii
  5.62 % 1548   Bacillus  sporothermodurans
  5.65 % 1551   Bacillus  badius
  5.79 % 1547   Bacillus  firmus
  5.85 % 1547   Bacillus  lentus
  5.90 % 1543   Bacillus  circulans
  5.95 % 1545   Bacillus  niacini
  6.30 % 1548   Bacillus  flexus
```

Neighbor Joining Tree

```
2.664 % ─────────────────────────────────
                              ┌─Bacillus lentus
                              ├─Bacillus firmus
                                 ┌─Bacillus flexus
                                 ├─Bacillus circulans
                                 └─Bacillus niacini
                              ┌─Bacillus oleronius
                              └─Bacillus sporothermodurans
                                 ┌─Bacillus badius
                                 └─Bacillus smithii
                                    ┌─C2461 6216-20 con
                                    └─Bacillus coagulans
```

Concise Alignment

```
                       1
              111222222241
              347011256784
              902967240204
```

C2461 6216-20 con TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)

Fig. 7

```
Alignment:     1549 C2462 6216-30 con
     0.65 %  1549   Bacillus coagulans
     4.84 %  1548   Bacillus oleronius
     5.36 %  1550   Bacillus smithii
     5.62 %  1548   Bacillus sporothermodurans
     5.65 %  1551   Bacillus badius
     5.79 %  1547   Bacillus firmus
     5.85 %  1547   Bacillus lentus
     5.90 %  1543   Bacillus circulans
     5.95 %  1545   Bacillus niacini
     6.30 %  1548   Bacillus flexus
```

Neighbor Joining Tree

2.664 %

```
              ┌─────────────── Bacillus lentus
          ┌───┤
          │   └────────────── Bacillus firmus
      ┌───┤       ┌────────────── Bacillus flexus
      │   │   ┌───┤
      │   └───┤   └───────────── Bacillus circulans
      │       └───────────────── Bacillus niacini
  ────┤           ┌──────────── Bacillus oleronius
      │       ┌───┤
      │       │   └─────────── Bacillus sporothermodurans
      │   ┌───┤       ┌──────── Bacillus badius
      └───┤   └───────┤
          │           └─────── Bacillus smithii
          └───────┐      ┌── C2462 6216-30 con
                  └──────┤
                         └── Bacillus coagulans
```
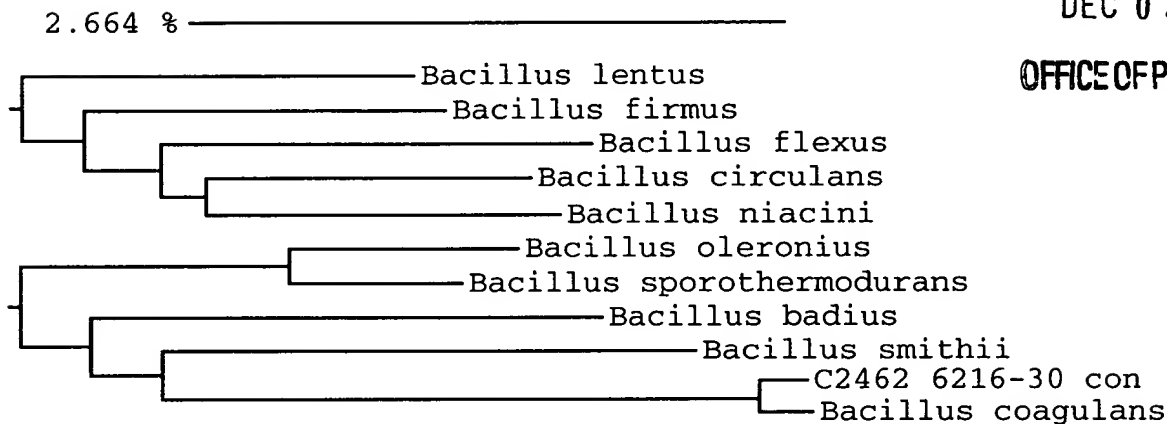
Concise Alignment

```
                       1
               111222222241
               347011256784
               902967240204
```

C2462 6216-30 con TCGAYTTWTTYC (SEQ ID NO:1; where r = A or G, y = C or T, and w = A or T)
Bacillus coagulans CTRGCGCACCCG (SEQ ID NO:2; where r = A or G, y = C or T, and w = A or T)

Fig. 8